

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Ashkenazi, Avi J.

(ii) TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

10 (iii) NUMBER OF SEQUENCES: 11

15 (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Genentech, Inc.
- (B) STREET: 460 Point San Bruno Blvd
- (C) CITY: South San Francisco
- (D) STATE: California
- (E) COUNTRY: USA
- (F) ZIP: 94080

20 (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: WinPatin (Genentech)

25 (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE: 31-Mar-1997
- (C) CLASSIFICATION:

30 (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Marschang, Diane L.
- (B) REGISTRATION NUMBER: 35,600
- (C) REFERENCE/DOCKET NUMBER: P1007R1

35 (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 415/225-5416  
(B) TELEFAX: 415/952-9881  
(C) TELEX: 910/371-7168

5 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids  
(B) TYPE: Amino Acid  
10 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu  
15 1 5 10 15

Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser  
20 20 25 30

20 Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu  
35 35 40 45

Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro  
50 50 55 60

25 Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln  
65 65 70 75

Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala  
30 80 85 90

Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu  
95 95 100 105

35 Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly

110 115 120

Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Ser Pro  
125 130 135

5

Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His  
140 145 150

Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys  
10 155 160 165

Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro  
170 175 180

154 Thr  
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(2) INFORMATION FOR SEQ ID NO:2:

200 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

250 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTGCTGGGGG CCCGGGCCAG NGGCGGCACT CGTAGCCCCA GGTGTGACTG 50

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TGCCGGTGAC TTCCACAAGA AGATTGGTCT GTTTGTTGC AGAGGCTGCC 100

CAGCGGGGCA ACTACCTGAA GGCCCCTTGC ACGGAGCCCT GCGCAACTCC 150

35

ACCTGCCTTG TGTGTCCCCA AGACACCTTC TTGGCCTGGG AGAACCCACCA 200

TAATTCTGAA TGTGCCCGCT GCCAGGCCTG TGATGAGCAG GCCTCCCAGG 250

TGGCGCTGGA GAACTGTTCA GCAGTGGCCG ACACCCGCTG TGGCTGTAAG 300

5 CAGGGCTGGT TTGTGGAGTG CCAGGGTCAG CCAATGTGTC AGCAGTTCA 350

CCCTTCTAAT GCCAACCATG CCTAGACTGC GGGGCCCTGC AACGCAACAC 400

ACGGCTAATN TGTTTCCCGC AGAGATNATT GTT 433

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CCCGCTGCCA GGCCTGTGAT GAGCAGGC 28

(2) INFORMATION FOR SEQ ID NO:4:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

35

CAGGGCCCCG CAGTCTAGGC ATGGTTGG 28

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- 5                   (A) LENGTH: 1438 base pairs  
                 (B) TYPE: Nucleic Acid  
                 (C) STRANDEDNESS: Single  
                 (D) TOPOLOGY: Linear

10                 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGGC GCGGAGGCCG AGAGAGAAGT CACTGCCCT GGCTCTACCT 50

TGAAGTGGTT CTCAGGGTTG GGGCGAGAGT CGGGGTGGGG ACCGAGATGC 100

15                 AGCTCTATCC TGTGCCCTG GTCGCAGCAG GCAGCCCAGC GCTTCGCGTG 150

TTCTACTTGG CCTGTCCGCT GCCGCCTAAT GAGCTCAGGT CTAGGCCGAG 200

20                 CAGAGGGGGC ACCTGGTCGG ACTCGGTTGG GCTCGGGCGG CCCCGCCTCC 250

CCCCGCCCGC CAGGCGGGCC CTTCTCGACG GCGCGGGGCG GGCCCTGCGG 300

GCGCGGGGCT GAAGGCGGAA CCACGACGGG CAGAGAGCAC GGAGCCGGGA 350

25                 AGCCCCTGGG CGCCCGTCGG AGGGCTATGG AGCAGCGGCC GCGGGGCTGC 400

GCGGCGGTGG CGGCGGCCGCT CCTCCTGGTG CTGCTGGGG CCCGGGCCA 450

30                 GGGCGGCACT CGTAGCCCCA GGTGTGACTG TGCCGGTGAC TTCCACAAGA 500

AGATTGGTCT GTTTGTTGC AGAGGCTGCC CAGCGGGGCA CTACCTGAAG 550

35                 GCCCTTGCA CGGAGCCCTG CGGCAACTCC ACCTGCCTTG TGTGTCCCCA 600

AGACACCTTC TTGGCCTGGG AGAACCAACCA TAATTCTGAA TGTGCCCGCT 650  
GCCAGGCCTG TGATGAGCAG GCCTCCCAGG TGGCGCTGGA GAACTGTTCA 700  
5 GCAGTGGCCG ACACCCGCTG TGGCTGTAAG CCAGGCTGGT TTGTGGAGTG 750  
CCAGGTCAGC CAATGTGTCA GCAGTTCACC CTTCTACTGC CAACCATGCC 800  
TAGACTGCGG GGCCCTGCAC CGCCACACAC GGCTACTCTG TTCCCGCAGA 850  
10 GATACTGACT GTGGGACCTG CCTGCCTGGC TTCTATGAAC ATGGCGATGG 900  
CTGCGTGTCC TGCCCCACGT AATTCTAGC TGTCGTGGGA TGGAGGGAAG 950  
15 GCGGGCTGGG AGCAGAGCAG GGGCCTGGGG TGGGGCAGGT GCTGCTGGTT 1000  
CAGGAATAGG AAGAGGGGAT AGGGAGGAGG GAGCCTTGGC CCTGTGATGG 1050  
20 GTGGGCCCA CTTCAGGCAA ACTTAGATGG CAAAAGAGCA ATCTGGATCC 1100  
GCCTTAGCCA GATACATAAG GGTATTTGCC TTCACTTTCA GCCAGCATTG 1150  
CCCCCAGCGA TCCTAGCCAG ATATTACAGA TGATTGTCA CTTACACAGA 1200  
25 GAGTCACATT GATATAGCTT TAAAACTTGG GCTGAAGGAG GTTGAGGCTG 1250  
CAGTGAGCTA TGATCGTGCC ACTGCACTTC AGCCTGGCA ACAGAGCGAG 1300  
ACCTATTAAA TAAATAAATA AATATTAAAT CTATTAAATA TTAAATATTA 1350  
30 AATCTATTAA ATAAATAAAT ACAAAAGGGCT GAGAGTCAGG ACTGTGCTGC 1400  
TAGTTCTCTA GGGGATCTTG GGCAAGTGCA GAGAATTG 1438

35 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 amino acids
- (B) TYPE: Amino Acid
- (C) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu  
1 5 10 15

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Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser  
20 25 30

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Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu  
35 40 45

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Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro  
50 55 60

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Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln  
65 70 75

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Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala  
80 85 90

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Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu  
95 100 105

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Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly  
110 115 120

Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Ser Pro  
125 130 135

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Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His

140 145 150

Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys  
155 160 165

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Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro  
170 175 180

10 Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala Ala Val Cys  
185 190 195

Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly Leu  
200 205 210

15 Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr Arg  
215 220 225

His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly  
230 235 240

20 Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu  
245 250 255

25 Asp Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys  
260 265 270

Ile Cys Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr  
275 280 285

30 Pro Glu Thr Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp  
290 295 300

Asp Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr  
305 310 315

35

Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met Met Leu Gln  
320 325 330

Pro Gly Pro Gln Leu Tyr Asp Val Met Asp Ala Val Pro Ala Arg  
5 335 340 345

Arg Trp Lys Glu Phe Val Arg Thr Leu Gly Leu Arg Glu Ala Glu  
350 355 360

10 Ile Glu Ala Val Glu Val Glu Ile Gly Arg Phe Arg Asp Gln Gln  
365 370 375

Tyr Glu Met Leu Lys Arg Trp Arg Gln Gln Pro Ala Gly Leu  
380 385 390

15 Gly Ala Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys  
395 400 405

20 Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro  
410 415 417

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCGCTCTGG TGGCCCTTGC AGAACGCC 27

35 (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - 5 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

10 TTCGGCCGAG AAGTTGAGAA ATGTC 25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- 15 (A) LENGTH: 1634 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGCCCTGC GGGCGCGGGG CTGAAGGCGG AACCACGACG GGCAGAGAGC 50

25 ACGGAGCCGG GAAGCCCCTG GGCGCCCGTC GGAGGGCT ATG GAG 94  
Met Glu

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CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG GCG CTC 133  
30 Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu

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CTC CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT 172  
Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr

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CGT AGC CCC AGG TGT GAC TGT GCC GGT GAC TTC CAC AAG 211  
 Arg Ser Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys  
     30                 35                 40

5     AAG ATT GGT CTG TTT TGT TGC AGA GGC TGC CCA GCG GGG 250  
 Lys Ile Gly Leu Phe Cys Cys Arg Gly Cys Pro Ala Gly  
     45                 50

10    CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC TGC GGC AAC 289  
 His Tyr Leu Lys Ala Pro Cys Thr Glu Pro Cys Gly Asn  
     55                 60                 65

15    TCC ACC TGC CTT GTG TGT CCC CAA GAC ACC TTC TTG GCC 328  
 Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala  
     70                 75                 80

20    TGG GAG AAC CAC CAT AAT TCT GAA TGT GCC CGC TGC CAG 367  
 Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln  
     85                 90

25    GCC TGT GAT GAG CAG GCC TCC CAG GTG GCG CTG GAG AAC 406  
 Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu Asn  
     95                 100              105

30    TGT TCA GCA GTG GCC GAC ACC CGC TGT GGC TGT AAG CCA 445  
 Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro  
     110              115

35    GGC TGG TTT GTG GAG TGC CAG GTC AGC CAA TGT GTC AGC 484  
 Gly Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser  
     120              125              130

40    AGT TCA CCC TTC TAC TGC CAA CCA TGC CTA GAC TGC GGG 523  
 Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly  
     135              140              145

GCC CTG CAC CGC CAC ACA CGG CTA CTC TGT TCC CGC AGA 562  
Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg  
150 155

5 GAT ACT GAC TGT GGG ACC TGC CTG CCT GGC TTC TAT GAA 601  
Asp Thr Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu  
160 165 170

10 CAT GGC GAT GGC TGC GTG TCC TGC CCC ACG AGC ACC CTG 640  
His Gly Asp Gly Cys Val Ser Cys Pro Thr Ser Thr Leu  
175 180

15 GGG AGC TGT CCA GAG CGC TGT GCC GCT GTC TGT GGC TGG 679  
Gly Ser Cys Pro Glu Arg Cys Ala Ala Val Cys Gly Trp  
185 190 195

20 AGG CAG ATG TTC TGG GTC CAG GTG CTC CTG GCT GGC CTT 718  
Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly Leu  
200 205 210

25 GTG GTC CCC CTC CTG CTT GGG GCC ACC CTG ACC TAC ACA 757  
Val Val Pro Leu Leu Gly Ala Thr Leu Thr Tyr Thr  
215 220

30 TAC CGC CAC TGC TGG CCT CAC AAG CCC CTG GTT ACT GCA 796  
Tyr Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala  
225 230 235

35 GAT GAA GCT GGG ATG GAG GCT CTG ACC CCA CCA CCG GCC 835  
Asp Glu Ala Gly Met Glu Ala Leu Thr Pro Pro Pro Ala  
240 245

40 ACC CAT CTG TCA CCC TTG GAC AGC GCC CAC ACC CTT CTA 874  
Thr His Leu Ser Pro Leu Asp Ser Ala His Thr Leu Leu  
250 255 260

	GCA CCT CCT GAC AGC AGT GAG AAG ATC TGC ACC GTC CAG	913	
	Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys Thr Val Gln		
	265	270	275
5	TTG GTG GGT AAC AGC TGG ACC CCT GGC TAC CCC GAG ACC	952	
	Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr		
	280	285	
10	CAG GAG GCG CTC TGC CCG CAG GTG ACA TGG TCC TGG GAC	991	
	Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp		
	290	295	300
15	CAG TTG CCC AGC AGA GCT CTT GGC CCC GCT GCT GCG CCC	1030	
	Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro		
	305	310	
20	ACA CTC TCG CCA GAG TCC CCA GCC GGC TCG CCA GCC ATG	1069	
	Thr Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met		
	315	320	325
25	ATG CTG CAG CCG GGC CCG CAG CTC TAC GAC GTG ATG GAC	1108	
	Met Leu Gln Pro Gly Pro Gln Leu Tyr Asp Val Met Asp		
	330	335	340
30	GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC ACG	1147	
	Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg Thr		
	345	350	
35	CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG	1186	
	Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val		
	355	360	365
	GAG ATC GGC CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC	1225	
	Glu Ile Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu		
	370	375	

AAG CGC TGG CGC CAG CAG CCC GCG GGC CTC GGA GCC 1264  
Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu Gly Ala  
380 385 390

5 GTT TAC GCG GCC CTG GAG CGC ATG GGG CTG GAC GGC TGC 1303  
   Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys  
           395                400                405

GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC CCG T 1340  
 10 Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro  
                   410                  415          417

GACACGGCGC CCACATTGCCA CCTAGGCGCT CTGGTGGCCC TTGCAGAAAGC 1390

154 CCTAAGTACG GTTACTTATG CGTGTAGACA TTTTATGTCA CTTATTAAAGC 1440

CGCTGGCACG GCCCTGCGTA GCAGCACCAG CCGGGCCCCAC CCCTGCTCGC 1490

CCCTATCGCT CCAGGCCAAGG CGAACGAAGCA CGAACCGAATG TCGAGAGGGGG 1540

GTGAAGACAT TTCTCAACTT CTCGGCCGGA GTTTGGCTGA GATCGCGGTA 1590

TTAAATCTGT GAAAGAAAAAC AAAAAAAAAAAA AAAAAAAAAAAA AAAAAA 1634

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: Nucleic Acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:11:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGATGGAA GTGTGTGATA TATCCTTGAT 30

15